

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/599,974C

1646

DATE: 07/29/98
 TIME: 10:06:50

INPUT SET: S27758.raw

This Raw Listing contains the General
 Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

- 1
- 2
- 3 (1) General Information:
- 4
- 5 (i) APPLICANT: Friedman, Jeffrey M.
- 6 Lee, Gwo-Hua
- 7 Proenca, Ricardo
- 8
- 9 (ii) TITLE OF INVENTION: DB, THE RECEPTOR FOR LEPTIN, NUCLEIC
- 10 ACIDS ENCODING THE RECEPTOR, AND USES THEREOF
- 11
- 12 (iii) NUMBER OF SEQUENCES: 56
- 13
- 14 (iv) CORRESPONDENCE ADDRESS:
- 15 (A) ADDRESSEE: David A. Jackson, Esq.
- 16 (B) STREET: 411 Hackensack Ave, Continental Plaza, 4th
- 17 Floor
- 18 (C) CITY: Hackensack
- 19 (D) STATE: New Jersey
- 20 (E) COUNTRY: USA
- 21 (F) ZIP: 07601
- 22
- 23 (v) COMPUTER READABLE FORM:
- 24 (A) MEDIUM TYPE: Floppy disk
- 25 (B) COMPUTER: IBM PC compatible
- 26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- 27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- 28
- 29 (vi) CURRENT APPLICATION DATA:
- 30 (A) APPLICATION NUMBER: US 08/599,974
- 31 (B) FILING DATE: 14-FEB-1996
- 32 (C) CLASSIFICATION:
- 33
- 34 (vii) PRIOR APPLICATION DATA:
- 35 (A) APPLICATION NUMBER: US 08/586,594
- 36 (B) FILING DATE: 16-JAN-1996
- 37 (C) CLASSIFICATION:
- 38
- 39 (viii) ATTORNEY/AGENT INFORMATION:
- 40 (A) NAME: Jackson Esq., David A.
- 41 (B) REGISTRATION NUMBER: 26,742
- 42 (C) REFERENCE/DOCKET NUMBER: 600-1-162 CP1
- 43
- 44 (ix) TELECOMMUNICATION INFORMATION:
- 45 (A) TELEPHONE: 201-487-5800
- 46 (B) TELEFAX: 201-343-1684

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/599,974CDATE: 07/29/98
TIME: 10:06:51

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47

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49 (2) INFORMATION FOR SEQ ID NO:1:

50

51 (i) SEQUENCE CHARACTERISTICS:

52 (A) LENGTH: 2529 base pairs

53 (B) TYPE: nucleic acid

54 (C) STRANDEDNESS: double

55 (D) TOPOLOGY: linear

56

57 (ii) MOLECULE TYPE: cDNA

58

59 (iii) HYPOTHETICAL: NO

60

61 (iv) ANTI-SENSE: NO

62

63

64 (vii) IMMEDIATE SOURCE:

65 (B) CLONE: A15 (OB-Ra)

66

67

68

69 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

70

71 GGGCTCAGGT CGGCGTCGTA CCAGCCGCTG AAGCGGTTCT CCAGGTTCCA GGCCTCTCG 60

72

73 CCATGCCGGA TCAGCACCAG CTTGTAGCTC GTGCCGAATT CGGCACGAGG TTGCTTTGGG 120

74

75 AATGAGCAAG GTCAAAACTG CTCTGCACTC ACAGACAACA CTGAAGGGAA GACACTGGCT 180

76

77 TCAGTAGTGA AGGCTTCAGT TTTTCGCCAG CTAGGTGTAA ACTGGGACAT AGAGTGCTGG 240

78

79 ATGAAAGGGG ACTTGACATT ATTCATCTGT CATATGGAGC CATTACCTAA GAACCCCTTC 300

80

81 AAGAATTATG ACTCTAAGGT CCATCTTTTA TATGATCTGC CTGAAGTCAT AGATGATTCG 360

82

83 CCTCTGCCCC CACTGAAAGA CAGCTTTCAG ACTGTCCAAT GCAACTGCAG TCTTCGGGGA 420

84

85 TGTGAATGTC ATGTGCCGGT ACCCAGAGCC AACTCAACT ACGCTCTTCT GATGTATTTG 480

86

87 GAAATCACAT CTGCCGGTGT GAGTTTTTCAG TCACCTCTGA TGTCAC TGCA GCCCATGCTT 540

88

89 GTTGTGAAAC CCGATCCACC CTTAGGTTTG CATATGGAAG TCACAGATGA TGGTAATTTA 600

90

91 AAGATTTCTT GGGACAGCCA AACAATGGCA CCATTTCCGC TTCAATATCA GGTGAAATAT 660

92

93 TTAGAGAATT CTACAATTGT AAGAGAGGCT GCTGAAATTG TCTCAGCTAC ATCTCTGCTG 720

94

95 GTAGACAGTG TGCTTCCTGG ATCTTCATAT GAGGTCCAGG TGAGGAGCAA GAGACTGGAT 780

96

97 GGTT CAGGAG TCTGGAGTGA CTGGAGTTCA CCTCAAGTCT TTACCACACA AGATGTTGTG 840

98

99 TATTTTCCAC CCAAATTCT GACTAGTGTT GGATCGAATG CTTCTTTTCA TTGCATCTAC 900

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100							
101	AAAAACGAAA	ACCAGATTAT	CTCCTCAAAA	CAGATAGTTT	GGTGGAGGAA	TCTAGCTGAG	960
102							
103	AAAAATCCCTG	AGATACAGTA	CAGCATTGTG	AGTGACCGAG	TTAGCAAAGT	TACCTTCTCC	1020
104							
105	AACCTGAAAG	CCACCAGACC	TCGAGGGAAG	TTTACCTATG	ACGCAGTGTA	CTGCTGCAAT	1080
106							
107	GAGCAGGCGT	GCCATCACCG	CTATGCTGAA	TTATACGTGA	TCGATGTCAA	TATCAATATA	1140
108							
109	TCATGTGAAA	CTGACGGGTA	CTTAACATAA	ATGACTTGCA	GATGGTCACC	CAGCACAATC	1200
110							
111	CAATCACTAG	TGGGAAGCAC	TGTGCAGCTG	AGGTATCACA	GGCGCAGCCT	GTATTGTCCCT	1260
112							
113	GATAGTCCAT	CTATTCATCC	TACGTCTGAG	CCCCAAAACT	GCGTCTTACA	GAGAGACGGC	1320
114							
115	TTTTATGAAT	GTGTTTTCCA	GCCAATCTTT	CTATTATCTG	GCTATACAAT	GTGGATCAGG	1380
116							
117	ATCAACCATT	CTTTAGGTTC	ACTTGACTCG	CCACCAACGT	GTGTCCCTTC	TGACTCCGTA	1440
118							
119	GTAAAACAC	TACCTCCATC	TAACGTAAAA	GCAGAGATTA	CTGTAAACAC	TGGATTATTG	1500
120							
121	AAAGTATCTT	GGGAAAAGCC	AGTCTTTCCG	GAGAATAACC	TTCAATTCCA	GATTTCGATAT	1560
122							
123	GGCTTAAGTG	GAAAAAGAAAT	ACAATGGAAG	ACACATGAGG	TATTCGATGC	AAAGTCAAAG	1620
124							
125	TCTGCCAGCC	TGCTGGTGTC	AGACCTCTGT	GCAGTCTATG	TGGTCCAGGT	TCGCTGCCGG	1680
126							
127	CGGTTGGATG	GACTAGGATA	TTGGAGTAAT	TGGAGCAGTC	CAGCCTATAC	GCTTGTCATG	1740
128							
129	GATGTAAAAG	TTCTTATGAG	AGGGCCTGAA	TTTTGGAGAA	AAATGGATGG	GGACGTTACT	1800
130							
131	AAAAAGGAGA	GAAATGTCAC	CTTGCTTTGG	AAGCCCCCTGA	CGAAAAATGA	CTCACTGTGT	1860
132							
133	AGTGTGAGGA	GGTACGTGGT	GAAGCATCGT	ACTGCCCACA	ATGGGACGTG	GTCAGAAGAT	1920
134							
135	GTGGGAAATC	GGACCAATCT	CACTTTCCCTG	TGGACAGAAC	CAGCGCACAC	TGTTACAGTT	1980
136							
137	CTGGCTGTCA	ATTCCCTCGG	CGCTTCCCTT	GTGAATTTTA	ACCTTACCTT	CTCATGGCCC	2040
138							
139	ATGAGTAAAG	TGAGTGCTGT	GGAGTCACTC	AGTGCTTATC	CCCTGAGCAG	CAGCTGTGTC	2100
140							
141	ATCCTTTTCT	GGACACTGTC	ACCTGATGAT	TATAGTCTGT	TATATCTGGT	TATTGAATGG	2160
142							
143	AAGATCCCTA	ATGAAGATGA	TGGAATGAAG	TGGCTTAGAA	TTCCCTCGAA	TGTTAAAAAG	2220
144							
145	TTTTATATCC	ACGATAATTT	TATTCCCATC	GAGAAATATC	AGTTTAGTCT	TTACCCAGTA	2280
146							
147	TTTATGGAAG	GAGTTGGAAG	ACCAAAGATA	ATTAATGGTT	TCACCAAAGA	TGCTATCGAC	2340
148							
149	AAGCAGCAGA	ATGACGCAGG	GCTGTATGTC	ATTGTACCCA	TAATTATTTT	CTCTTGTGTC	2400
150							
151	CTACTGCTCG	GAACACTGTT	AATTTACAC	CAGAGAATGA	AAAAGTTGTT	TTGGGACGAT	2460
152							

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153 GTTCCAAACC CCAAGAATTG TTCCTGGGCA CAAGGACTGA ATTTCCAAAA GAGAACGGAC 2520

154

155 ACTCTTTGA

2529

156

157 (2) INFORMATION FOR SEQ ID NO:2:

158

159 (i) SEQUENCE CHARACTERISTICS:

160 (A) LENGTH: 842 amino acids

161 (B) TYPE: amino acid

162 (C) STRANDEDNESS: Not Relevant

163 (D) TOPOLOGY: Not Relevant

164

165 (ii) MOLECULE TYPE: protein

166

167 (iii) HYPOTHETICAL: NO

168

169 (iv) ANTI-SENSE: NO

170

171

172 (vii) IMMEDIATE SOURCE:

173 (B) CLONE: OB-Ra

174

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176

177 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

178

179 Gly Leu Arg Ser Ala Ser Tyr Gln Pro Leu Lys Arg Phe Ser Arg Phe
180 1 5 10 15

181

182 Gln Ala Leu Ser Pro Cys Arg Ile Ser Thr Ser Leu Xaa Leu Val Pro
183 20 25 30

184

185 Asn Ser Ala Arg Gly Cys Phe Gly Asn Glu Gln Gly Gln Asn Cys Ser
186 35 40 45

187

188 Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala Ser Val Val Lys
189 50 55 60

190

191 Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp Ile Glu Cys Trp
192 65 70 75 80

193

194 Met Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met Glu Pro Leu Pro
195 85 90 95

196

197 Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His Leu Leu Tyr Asp
198 100 105 110

199

200 Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Pro Leu Lys Asp Ser
201 115 120 125

202

203 Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly Cys Glu Cys His
204 130 135 140

205

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206	Val	Pro	Val	Pro	Arg	Ala	Lys	Leu	Asn	Tyr	Ala	Leu	Leu	Met	Tyr	Leu
207	145					150					155					160
208																
209	Glu	Ile	Thr	Ser	Ala	Gly	Val	Ser	Phe	Gln	Ser	Pro	Leu	Met	Ser	Leu
210					165					170					175	
211																
212	Gln	Pro	Met	Leu	Val	Val	Lys	Pro	Asp	Pro	Pro	Leu	Gly	Leu	His	Met
213				180					185					190		
214																
215	Glu	Val	Thr	Asp	Asp	Gly	Asn	Leu	Lys	Ile	Ser	Trp	Asp	Ser	Gln	Thr
216			195					200					205			
217																
218	Met	Ala	Pro	Phe	Pro	Leu	Gln	Tyr	Gln	Val	Lys	Tyr	Leu	Glu	Asn	Ser
219		210					215					220				
220																
221	Thr	Ile	Val	Arg	Glu	Ala	Ala	Glu	Ile	Val	Ser	Ala	Thr	Ser	Leu	Leu
222	225					230					235					240
223																
224	Val	Asp	Ser	Val	Leu	Pro	Gly	Ser	Ser	Tyr	Glu	Val	Gln	Val	Arg	Ser
225					245					250					255	
226																
227	Lys	Arg	Leu	Asp	Gly	Ser	Gly	Val	Trp	Ser	Asp	Trp	Ser	Ser	Pro	Gln
228			260						265					270		
229																
230	Val	Phe	Thr	Thr	Gln	Asp	Val	Val	Tyr	Phe	Pro	Pro	Lys	Ile	Leu	Thr
231			275					280					285			
232																
233	Ser	Val	Gly	Ser	Asn	Ala	Ser	Phe	His	Cys	Ile	Tyr	Lys	Asn	Glu	Asn
234		290					295					300				
235																
236	Gln	Ile	Ile	Ser	Ser	Lys	Gln	Ile	Val	Trp	Trp	Arg	Asn	Leu	Ala	Glu
237	305					310					315					320
238																
239	Lys	Ile	Pro	Glu	Ile	Gln	Tyr	Ser	Ile	Val	Ser	Asp	Arg	Val	Ser	Lys
240					325					330					335	
241																
242	Val	Thr	Phe	Ser	Asn	Leu	Lys	Ala	Thr	Arg	Pro	Arg	Gly	Lys	Phe	Thr
243				340					345					350		
244																
245	Tyr	Asp	Ala	Val	Tyr	Cys	Cys	Asn	Glu	Gln	Ala	Cys	His	His	Arg	Tyr
246			355					360					365			
247																
248	Ala	Glu	Leu	Tyr	Val	Ile	Asp	Val	Asn	Ile	Asn	Ile	Ser	Cys	Glu	Thr
249		370					375					380				
250																
251	Asp	Gly	Tyr	Leu	Thr	Lys	Met	Thr	Cys	Arg	Trp	Ser	Pro	Ser	Thr	Ile
252	385					390					395					400
253																
254	Gln	Ser	Leu	Val	Gly	Ser	Thr	Val	Gln	Leu	Arg	Tyr	His	Arg	Arg	Ser
255					405					410					415	
256																
257	Leu	Tyr	Cys	Pro	Asp	Ser	Pro	Ser	Ile	His	Pro	Thr	Ser	Glu	Pro	Lys
258				420					425					430		

PAGE: 1

SEQUENCE VERIFICATION REPORT
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Original Text